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OCT 10 2002

SEQUENCE LISTING

TECH CENTER 1600/2900

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Levitan, Diane

<120> IDENTIFICATION OF SEL 12 AND USES THEREOF

<130> 0575/48231-A-PCT-US

<140> 09/043,944

<141> 1998-03-27

<150> PCT/US96/15727

<151> 1996-09-27

<150> 60/004,387

<151> 1995-09-27

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 461

<212> PRT

<213> C. elegans

<220>

<221> misc_feature

<223> Fig. 1A

<400> 1

Met Pro Ser Thr Arg Arg Gln Gln Glu Gly Gly Gly Ala Asp Ala Glu

1

5

10

15

Thr His Thr Val Tyr Gly Thr Asn Leu Ile Thr Asn Arg Asn Ser Gln
20 25 30

Glu Asp Glu Asn Val Val Glu Glu Ala Glu Leu Lys Tyr Gly Ala Ser
35 40 45

His Val Ile His Leu Phe Val Pro Val Ser Leu Cys Met Ala Leu Val
50 55 60

Val Phe Thr Met Asn Thr Ile Thr Phe Tyr Ser Gln Asn Asn Gly Arg
65 70 75 80

His Leu Leu Ser His Pro Phe Val Arg Glu Thr Asp Ser Ile Val Glu
85 90 95

Lys Gly Leu Met Ser Leu Gly Asn Ala Leu Val Met Leu Cys Val Val
100 105 110

Val Leu Met Thr Val Leu Leu Ile Val Phe Tyr Lys Tyr Lys Phe Tyr
115 120 125

Lys Leu Ile His Gly Trp Leu Ile Val Ser Ser Phe Leu Leu Leu Phe
130 135 140

Leu Phe Thr Thr Ile Tyr Val Gln Glu Val Leu Lys Ser Phe Asp Val
145 150 155 160

Ser Pro Ser Ala Leu Leu Val Leu Phe Gly Leu Gly Asn Tyr Gly Val
165 170 175

Leu Gly Met Met Cys Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln
180 185 190

Phe Tyr Leu Ile Thr Met Ser Ala Leu Met Ala Leu Val Phe Ile Lys
195 200 205

Tyr Leu Pro Glu Trp Thr Val Trp Phe Val Leu Phe Val Ile Ser Val
210 215 220

Trp Asp Leu Val Ala Val Leu Thr Pro Lys Gly Pro Leu Arg Tyr Leu
225 230 235 240

Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile Phe Pro Ala Leu Ile
245 250 255

Tyr Ser Ser Gly Val Ile Tyr Pro Tyr Val Leu Val Thr Ala Val Glu
260 265 270

Asn Thr Thr Asp Pro Arg Glu Pro Thr Ser Ser Asp Ser Asn Thr Ser
275 280 285

Thr Ala Phe Pro Gly Glu Ala Ser Cys Ser Ser Glu Thr Pro Lys Arg
290 295 300

Pro Lys Val Lys Arg Ile Pro Gln Lys Val Gln Ile Glu Ser Asn Thr
305 310 315 320

Thr Ala Ser Thr Thr Gln Asn Ser Gly Val Arg Val Glu Arg Glu Leu
325 330 335

Ala Ala Glu Arg Pro Thr Val Gln Asp Ala Asn Phe His Arg His Glu
340 345 350

Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile Phe Tyr
355 360 365

Ser Val Leu Leu Gly Lys Ala Ser Ser Tyr Phe Asp Trp Asn Thr Thr
370 375 380

Ile Ala Cys Tyr Val Ala Ile Leu Ile Gly Leu Cys Phe Thr Leu Val
385 390 395 400

Leu Leu Ala Val Phe Lys Arg Ala Leu Pro Ala Leu Gln Phe Pro Phe
405 410 415

Ser Pro Asp Ser Phe Phe Thr Phe Val Pro Ala Gly Ser Ser Pro His
420 425 430

Leu Leu His Lys Ser Leu Lys Ser Val Tyr Tyr Ile Asn Ser Leu Phe
435 440 445

Leu Pro Phe Leu Cys Ile Ile Asn Phe Ser Ile Ile Ser
450 455 460

<210> 2
<211> 467

<212> PRT
<213> human

<220>
<221> misc_feature
<223> Fig. 2A S182

<400> 2

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

<210> 3
<211> 157
<212> PRT
<213> C. elegans

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> unknown amino acid

<400> 3

Glu Gly Lys Ser Pro Ser Asn Thr Glu Arg Xaa Val Ile Met Leu Phe
1 5 10 15

Val Pro Val Thr Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser
20 25 30

Val Arg Phe Tyr Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe

35

40

45

Thr Glu Asp Thr Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu
50 55 60

Asn Thr Leu Ile Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu
65 70 75 80

Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu
85 90 95

Ile Met Ser Ser Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu
100 105 110

Gly Glu Val Leu Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu
115 120 125

Leu Leu Thr Val Trp Glu Leu Arg Gly Ser Gly His Gly Val His Pro
130 135 140

Leu Glu Gly Ala Phe Gly Ala Ala Glu Ala Tyr Leu Ser
145 150 155

<210> 4

<211> 465

<212> PRT

<213> C. elegans

<220>

<221> misc_feature

<223> Fig. 2A SPE-4

<400> 4

Met Asp Thr Leu Arg Ser Ile Ser Ser Glu Leu Val Arg Ser Ser Gln
1 5 10 15

Leu Arg Trp Thr Leu Phe Ser Val Ile Ala Asn Met Ser Leu Thr Leu
20 25 30

Ser Ile Trp Ile Gly Val Tyr Asn Met Glu Val Asn Ser Glu Leu Ser
35 40 45

Lys Thr Tyr Phe Leu Asp Pro Ser Phe Glu Gln Thr Thr Gly Asn Leu
50 55 60

Leu Leu Asp Gly Phe Ile Asn Gly Val Gly Thr Ile Leu Val Leu Gly
65 70 75 80

Cys Val Ser Phe Ile Met Leu Ala Phe Val Leu Phe Asp Phe Arg Arg
85 90 95

Ile Val Lys Ala Trp Leu Thr Leu Ser Cys Leu Leu Ile Leu Phe Gly
100 105 110

Val Ser Ala Gln Thr Leu His Asp Met Phe Ser Gln Val Phe Asp Gln
115 120 125

Asp Asp Asn Asn Gln Tyr Tyr Met Thr Ile Val Leu Ile Val Val Pro

130

135

140

Thr Val Val Tyr Gly Phe Gly Gly Ile Tyr Ala Phe Phe Ser Asn Ser
145 150 155 160

Ser Leu Ile Leu His Gln Ile Phe Val Val Thr Asn Cys Ser Leu Ile
165 170 175

Ser Val Phe Tyr Leu Arg Val Phe Pro Ser Lys Thr Thr Trp Phe Val
180 185 190

Leu Trp Ile Val Leu Phe Trp Asp Leu Phe Ala Val Leu Ala Pro Met
195 200 205

Gly Pro Leu Lys Lys Val Gln Glu Lys Ala Ser Asp Tyr Ser Lys Cys
210 215 220

Val Leu Asn Leu Ile Met Phe Ser Ala Asn Glu Lys Arg Leu Thr Ala
225 230 235 240

Gly Ser Asn Gln Glu Glu Thr Asn Glu Gly Glu Glu Ser Thr Ile Arg
245 250 255

Arg Thr Val Lys Gln Thr Ile Glu Tyr Tyr Thr Lys Arg Glu Ala Gln
260 265 270

Asp Asp Glu Phe Tyr Gln Lys Ile Arg Gln Arg Arg Ala Ala Ile Asn
275 280 285

Pro Asp Ser Val Pro Thr Glu His Ser Pro Leu Val Glu Ala Glu Pro
290 295 300

Ser Pro Ile Glu Leu Lys Glu Lys Asn Ser Thr Glu Glu Leu Ser Asp
305 310 315 320

Asp Glu Ser Asp Thr Ser Glu Thr Ser Ser Gly Ser Ser Asn Leu Ser
325 330 335

Ser Ser Asp Ser Ser Thr Thr Val Ser Thr Ser Asp Ile Ser Thr Ala
340 345 350

Glu Glu Cys Asp Gln Lys Glu Trp Asp Asp Leu Val Ser Asn Ser Leu
355 360 365

Pro Asn Asn Asp Lys Arg Pro Ala Thr Ala Ala Asp Ala Leu Asn Asp
370 375 380

Gly Glu Val Leu Arg Leu Gly Phe Gly Asp Phe Val Phe Tyr Ser Leu
385 390 395 400

Leu Ile Gly Gln Ala Ala Ala Ser Gly Cys Pro Phe Ala Val Ile Ser
405 410 415

Ala Ala Leu Gly Ile Leu Phe Gly Leu Val Val Thr Leu Thr Val Phe
420 425 430

Ser Thr Glu Glu Ser Thr Thr Pro Ala Leu Pro Leu Pro Val Ile Cys

435

440

445

Gly Thr Phe Cys Tyr Phe Ser Ser Met Phe Phe Trp Glu Gln Leu Tyr

450

455

460

Gly

465

<210> 5

<211> 1500

<212> DNA

<213> C. elegans

<220>

<221> misc_feature

<223> Fig. 1A

<400> 5

gtttaattac ccaagtttga gatgccttcc|aca|aggagac aacaggaggg cggaggtgca 60

gatgcggaaa cacataccgt ttacggtaca aatctgataa caaatcggaa tagccaagaa 120

gacgaaaatg ttgtggaaga agcggagctg aaatacggag catctcacgt tattcatcta 180

tttgtgccgg tgtcactatg catggctctg gttgttttta cgatgaacac gattacgttt 240

tatagtcaaa acaatggaag gcatttacta tcacatcctt ttgtccggga aacagacagt 300

atcgttgaga agggattgat gtcacttga aatgctctcg tcatgtttgtg cgtgggtcgtt 360

ctgatgacag ttctgctgat tgttttctat aaatacaagt ttataagct tattcatgga 420

tggcttattg tcagcagttt tcttcttctt ttcctattca ctacaatcta tgtgcaagaa 480

gttctgaaaa gtttcgatgt gtctcccagc gcactattgg ttttgtttgg actgggtaac	540
tatggagttc tcggaatgat gtgtatacat tggaaaggtc cattgcgtct gcaacagttc	600
taccttatta caatgtctgc actaatggct ctggtcttta tcaagtacct accagaatgg	660
actgtgtggt ttgtgctggt tggtatctcg gtttgggato tggttgccgt gctcacacca	720
aaaggaccat tgagatatatt ggtggaaact gcacaggaga gaaacgagcc aattttcccg	780
gcgctgattt attcgtctgg agtcatctat ccctacgttc ttgttactgc agttgaaaac	840
acgacagacc cccgtgaacc gacgtcgtca gactcaaata cttctacagc ttttcctgga	900
gaggcgagtt gttcatctga aacgccaaaa cggccaaaag tgaaacgaat tcctcaaaaa	960
gtgcaaatcg aatcgaatac tacagcttca acgacacaaa actctggagt aagggtggaa	1020
cgggagctag ctgctgagag accaactgta caagacgcca attttcacag gcacgaagag	1080
gaagagagag gtgtgaaact tggctctgggc gacttcattt tctactctgt tctcctcggc	1140
aaggcttcat cgtactttga ctggaacacg actatcgctt gttatgtggc cattcttata	1200
ggtctctgct tcaactctgt cctgctcgcc gtcttcaaac gagcaactccc ggctctgcaa	1260
tttccatttt ctccggactc attttttact tttgtaccgg ctggatcata accccatttg	1320
ttacacaagt ctctcaaaag tgtttattat attaattctc tgtttttgcc atttctttgc	1380
atcatcaact ttctgattat atcttgagcg atctcaaagc tttattttac atacctattt	1440
atttttgaac tttgtcattt aagttatata aataatttat taaaaaaaaa aaaaaaaaaa	1500

<210> 6
 <211> 461
 <212> PRT

<213> C. elegans

<220>

<221> misc_feature

<223> Fig. 2A Sel-12

<400> 6

Met Pro Ser Thr Arg Arg Gln Gln Glu Gly Gly Gly Ala Asp Ala Glu
1 5 10 15

Thr His Thr Val Tyr Gly Thr Asn Leu Ile Thr Asn Arg Asn Ser Gln
20 25 30

Glu Asp Glu Asn Val Val Glu Glu Ala Glu Leu Lys Tyr Gly Ala Ser
35 40 45

His Val Ile His Leu Phe Val Pro Val Ser Leu Cys Met Ala Leu Val
50 55 60

Val Phe Thr Met Asn Thr Ile Thr Phe Tyr Ser Gln Asn Asn Gly Arg
65 70 75 80

His Leu Leu Ser His Pro Phe Val Arg Glu Thr Asp Ser Ile Val Glu
85 90 95

Lys Gly Leu Met Ser Leu Gly Asn Ala Leu Val Met Leu Cys Val Val
100 105 110

Val Leu Met Thr Val Leu Leu Ile Val Phe Tyr Lys Tyr Lys Phe Tyr

115		120		125											
Lys	Leu	Ile	His	Gly	Trp	Leu	Ile	Val	Ser	Ser	Phe	Leu	Leu	Leu	Phe
130		135		140											
Leu	Phe	Thr	Thr	Ile	Tyr	Val	Gln	Glu	Val	Leu	Lys	Ser	Phe	Asp	Val
145				150						155				160	
Ser	Pro	Ser	Ala	Leu	Leu	Val	Leu	Phe	Gly	Leu	Gly	Asn	Tyr	Gly	Val
			165						170					175	
Leu	Gly	Met	Met	Cys	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln
		180						185					190		
Phe	Tyr	Leu	Ile	Thr	Met	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys
	195						200						205		
Tyr	Leu	Pro	Glu	Trp	Thr	Val	Trp	Phe	Val	Leu	Phe	Val	Ile	Ser	Val
210						215					220				
Trp	Asp	Leu	Val	Ala	Val	Leu	Thr	Pro	Lys	Gly	Pro	Leu	Arg	Tyr	Leu
225			230							235				240	
Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Pro	Ile	Phe	Pro	Ala	Leu	Ile
			245						250					255	
Tyr	Ser	Ser	Gly	Val	Ile	Tyr	Pro	Tyr	Val	Leu	Val	Thr	Ala	Val	Glu
		260						265					270		

Asn Thr Thr Asp Pro Arg Glu Pro Thr Ser Ser Asp Ser Asn Thr Ser
275 280 285

Thr Ala Phe Pro Gly Glu Ala Ser Cys Ser Ser Glu Thr Pro Lys Arg
290 295 300

Pro Lys Val Lys Arg Ile Pro Gln Lys Val Gln Ile Glu Ser Asn Thr
305 310 315 320

Thr Ala Ser Thr Thr Gln Asn Ser Gly Val Arg Val Glu Arg Glu Leu
325 330 335

Ala Ala Glu Arg Pro Thr Val Gln Asp Ala Asn Phe His Arg His Glu
340 345 350

Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile Phe Tyr
355 360 365

Ser Val Leu Leu Gly Lys Ala Ser Ser Tyr Phe Asp Trp Asn Thr Thr
370 375 380

Ile Ala Cys Tyr Val Ala Ile Leu Ile Gly Leu Cys Phe Thr Leu Val
385 390 395 400

Leu Leu Ala Val Phe Lys Arg Ala Leu Pro Ala Leu Gln Phe Pro Phe
405 410 415

Ser Pro Asp Ser Phe Phe Thr Phe Val Pro Ala Gly Ser Ser Pro His

420

425

430

Leu Leu His Lys Ser Leu Lys Ser Val Tyr Tyr Ile Asn Ser Leu Phe

435

440

445

Leu Pro Phe Leu Cys Ile Ile Asn Phe Ser Ile Ile Ser

450

455

460

<210> 7

<211> 21

<212> DNA

<213> C. elegans

<220>

<221> artificial_sequence

<222> (1)..(21)

<223> primer or probe

<400> 7

tgtctgagtt actagttttc c

21

<210> 8

<211> 24

<212> DNA

<213> C. elegans

<220>

<221> artificial_sequence

<222> (1)..(24)

<223> primer or probe

<400> 8

ggaatctgaa gcacctgtaa gcat

24

<210> 9

<211> 448

<212> PRT

<213> human

<220>

<221> misc_feature

<223> Fig. 2A E5-1

<220>

<221> misc_feature

<223> Fig. 2A E5-1/STM2

<400> 9

Met	Leu	Thr	Phe	Met	Ala	Ser	Asp	Ser	Glu	Glu	Glu	Val	Cys	Asp	Glu
1				5					10					15	

Arg	Thr	Ser	Leu	Met	Ser	Ala	Glu	Ser	Pro	Thr	Pro	Arg	Ser	Cys	Gln
			20					25					30		

Glu	Gly	Arg	Gln	Gly	Pro	Glu	Asp	Gly	Glu	Asn	Thr	Ala	Gln	Trp	Arg
		35					40					45			

Ser	Gln	Glu	Asn	Glu	Glu	Asp	Gly	Glu	Glu	Asp	Pro	Asp	Arg	Tyr	Val
	50					55					60				

Cys	Ser	Gly	Val	Pro	Gly	Arg	Pro	Pro	Gly	Leu	Glu	Glu	Glu	Leu	Thr
65					70					75				80	

Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
85 90 95

Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
100 105 110

Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
115 120 125

Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
130 135 140

Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
145 150 155 160

Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
165 170 175

Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
180 185 190

Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
195 200 205

Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
210 215 220

Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
225 230 235 240

Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
245 250 255

Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
260 265 270

Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
275 280 285

Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
290 295 300

Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
305 310 315 320

Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
325 330 335

Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
340 345 350

Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
355 360 365

Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
370 375 380

Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
385 390 395 400

Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
405 410 415

Pro Ile Ser Thr Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
420 425 430

Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
435 440 445

<210> 10

<211> 27

<212> DNA

<213> human

<220>

<221> artifical_sequence

<222> (1)..(27)

<223> sense primer for human PS1; pg 52

<400> 10

ggggtaccat gacagagtta cctgcac

27

<210> 11

<211> 25

<212> DNA

<213> human

<220>
<221> artificial_sequence
<222> (1)..(25)
<223> antisense primer for human PS1; pg. 52

<400> 11
ccgggatcca tgggattcta accgc

25

<210> 12
<211> 27
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(27)
<223> PS1 M146L sense primer 1

<400> 12
gtcattgttg tcttgactat cctcctg

27

<210> 13
<211> 20
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(20)
<223> PS1 M146L antisense primer 1

<400> 13
gaggagtaaa tgagagctgg

20

<210> 14
<211> 27
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(27)
<223> PS1 M146L sense primer 2

<400> 14
caggaggata gtcaggacaa caatgac

27

<210> 15
<211> 19
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(19)
<223> PS1 M146L antisense primer 2

<400> 15
caggtggtgg agcaagatg

19

<210> 16
<211> 20
<212> DNA
<213> human

<220>

<221> artificial_sequence
<222> (1)..(20)
<223> PS1 H163R primer

<400> 16
ctaggtcatc cgtgcctggc

20

<210> 17
<211> 20
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(20)
<223> PS1 H163R primer

<400> 17
gccaggcacg gatgacctag

20

<210> 18
<211> 26
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(26)
<223> PS1 L286V primer

<400> 18
cgctttttcc agctgtcatt tactcc

26

<210> 19
<211> 27
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(27)
<223> PS1 L286V primer

<400> 19
ccggaattct caggttgtgt tccagtc

27

<210> 20
<211> 26
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(26)
<223> PS1 L286V primer

<400> 20
ggagtaaattg acagctggaa aaagcg

26

<210> 21
<211> 24
<212> DNA
<213> human

<220>
<221> artificial_sequence

<222> (1)..(24)

<223> PS1 L286V primer

<400> 21

ggatccattg ttgtcatgac tatc

24

<210> 22

<211> 23

<212> DNA

<213> human

<220>

<221> artificial_sequence

<222> (1)..(23)

<223> PS1 C410Y primer

<400> 22

caaccatagc ctatttcgta gcc

23

<210> 23

<211> 33

<212> DNA

<213> human

<220>

<221> artificial_sequence

<222> (1)..(33)

<223> PS1 C410Y primer

<400> 23

gccagtgaat tgtaatacga ctactatag ggc

33

<210> 24
<211> 23
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(23)
<223> PS1 C410Y primer

<400> 24
ggctacgaaa taggctatgg ttg

23

<210> 25
<211> 24
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(24)
<223> PS1 C410Y primer

<400> 25
ccggaattct gaatggactg cgtg

24

<210> 26
<211> 27
<212> DNA
<213> human

<220>
<221> artificial_sequence
<222> (1)..(27)

<223> PS2 primer

<400> 26

ccggtaccaa gtgttcgtgg tgcttcc

27

<210> 27

<211> 29

<212> DNA

<213> human

<220>

<221> artificial_sequence

<222> (1)..(29)

<223> PS2 primer

<400> 27

ccgtctagac ctcagatgta gagctgatg

29
